STAT 5443, FINAL PROJECT

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PART 1

Sparse Classification

Comparing penalized methods for High-dimensional Classification

We would like to compare the performance of several modern regression methods including penalized regression methods such as LASSO and Elastic Net regression with 10-fold cross-validation.

Library hdrm was installed following the directions from: https://github.com/pbreheny/hdrm

```
library(hdrm)
```

```
## Loading required package: glmnet

## Loading required package: Matrix

## Loaded glmnet 4.0-2

## Loading required package: ncvreg
```

```
library(glmnet)
library(ggplot2)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --

## v tibble  3.0.4     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
## v purrr   0.3.4

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x tidyr::pack()   masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
```

```
library(caret)
```

```
## Loading required package: lattice
```

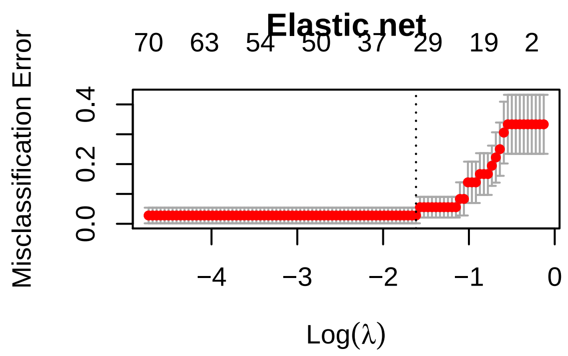
```
##
## Attaching package: 'caret'
```

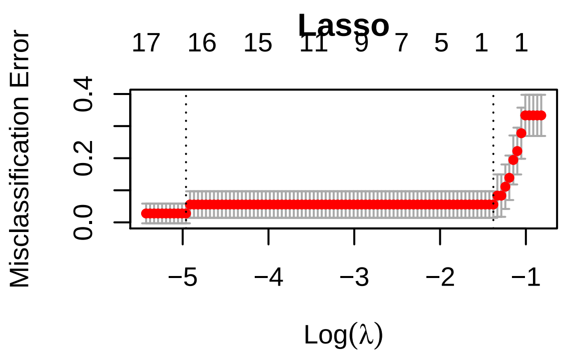
```
## The following object is masked from 'package:purrr':
##
##     lift
```

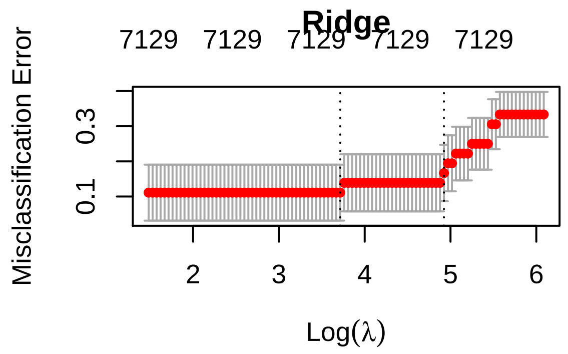
```
downloadData(Golub1999)
attachData(Golub1999)
```

```
n=nrow(X)

#split in train and test sets
set.seed(1234)
train_rows <- sample(1:n, n/2)
X.train <- X[train_rows, ]
X.test <- X[-train_rows, ]

y.train <- y[train_rows]
y.test <- y[-train_rows]
```

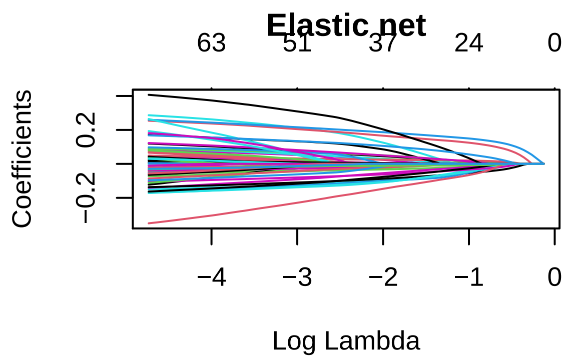
```
#cross validation

alpha=0.5
#Using cross validation for best lambda in all models
fit.elastic_net<-cv.glmnet(X.train,y.train,family="binomial",type.measure = "class",alpha=alpha)
fit.lasso<-cv.glmnet(X.train,y.train,family="binomial",type.measure = "class",alpha=1)
fit.ridge<-cv.glmnet(X.train,y.train,family="binomial",type.measure = "class",alpha=0)
par(mfrow=c(2,2))
plot(fit.elastic_net, main="Elastic net")
plot(fit.lasso, main="Lasso")
plot(fit.ridge, main="Ridge")
par(mfrow=c(1,1))
```

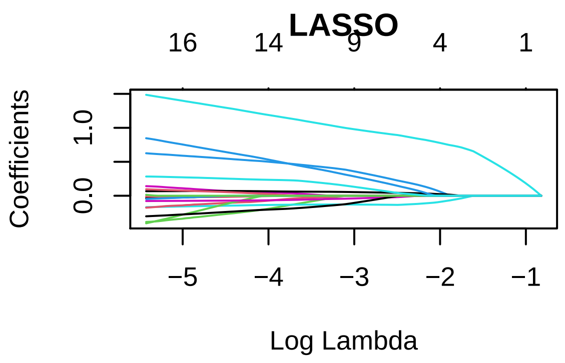


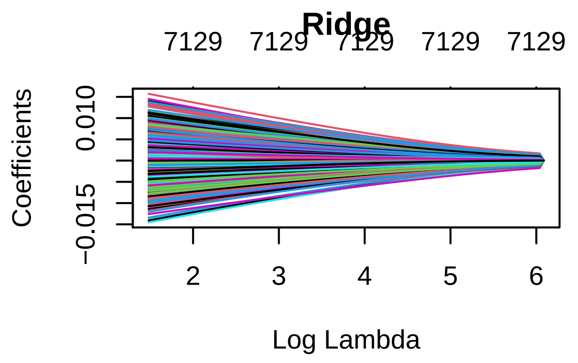




```r
#Solution paths
par(mfrow=c(2,2))
plot(fit.elastic_net$glmnet.fit,xvar="lambda", main="Elastic net")
plot(fit.lasso$glmnet.fit,xvar="lambda",main="LASSO")
plot(fit.ridge$glmnet.fit,xvar="lambda",main="Ridge")
```



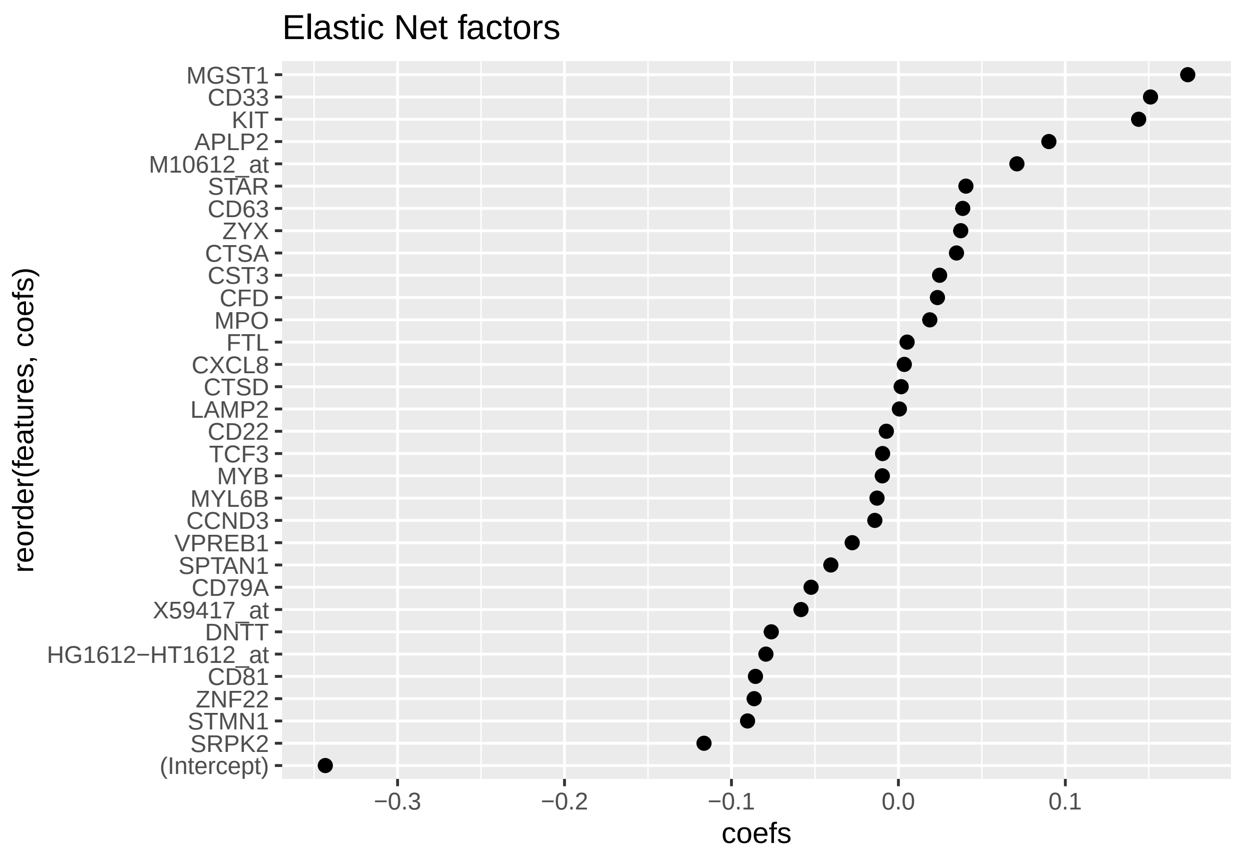




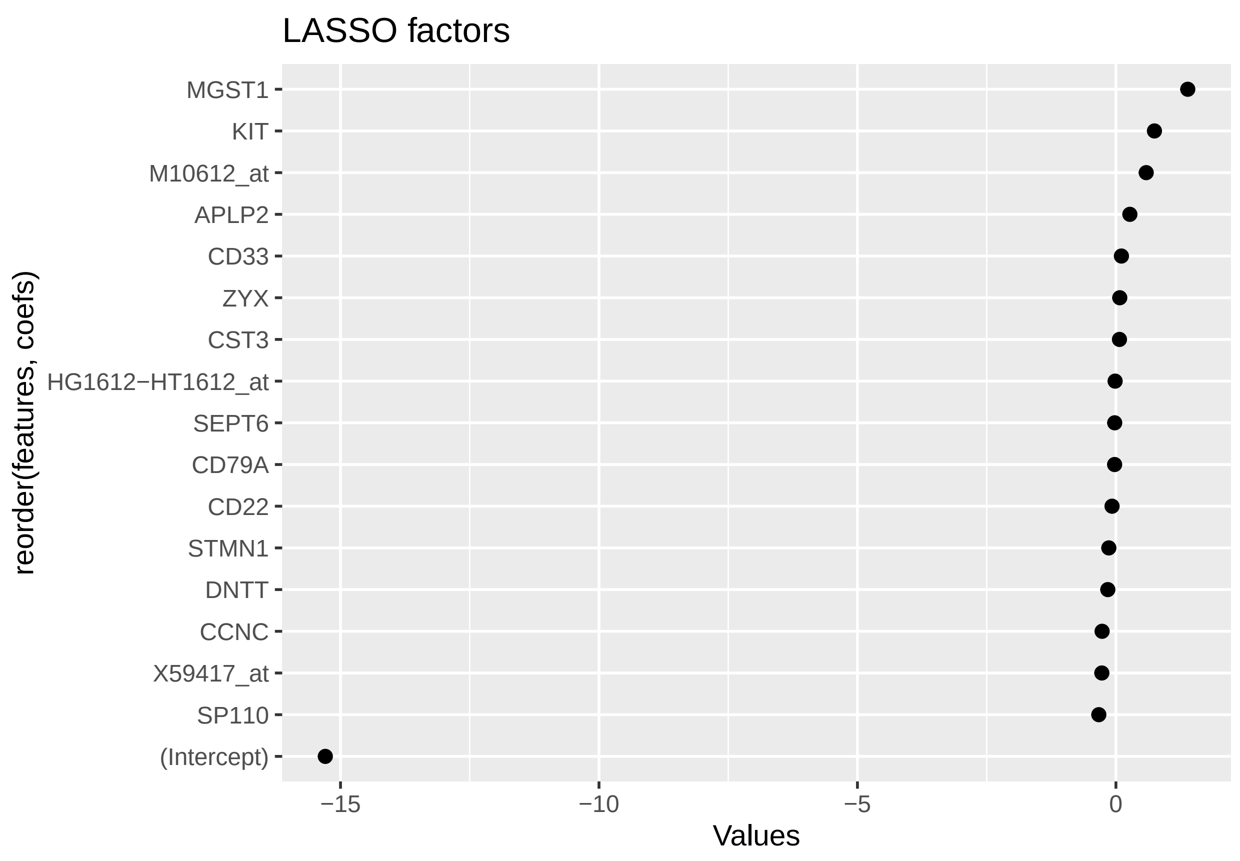
The solution paths are very crowded for the elastic net and ridge regression. Non-zero coefficients will be extracted and sorted in descending order.Because the number of coefficients for Ridge Regression is too high (~7130) only the first 50 will be used for plotting purposes.

```
#making dataframes from the non-zero coefficients
coef.enet<-coef(fit.elastic_net,s="lambda.min")
coef.enet <- data.frame(
  features = coef.enet@Dimnames[[1]][ which(coef.enet != 0 ) ],
  coefs    = coef.enet              [ which(coef.enet != 0 ) ]
)

coef.lasso<-coef(fit.lasso,s="lambda.min")
coef.lasso <- data.frame(
  features = coef.lasso@Dimnames[[1]][ which(coef.lasso != 0 ) ],
  coefs    = coef.lasso              [ which(coef.lasso != 0 ) ]
)

coef.ridge<-coef(fit.ridge,s="lambda.min")
coef.ridge <- data.frame(
  features = coef.ridge@Dimnames[[1]][ which(coef.ridge != 0 ) ],
  coefs    = coef.ridge              [ which(coef.ridge != 0 ) ]
)

#Sorting in decreasing order

#Because the number of coefficients for Ridge Regression is too high (~7130) only the first 50 will be
```

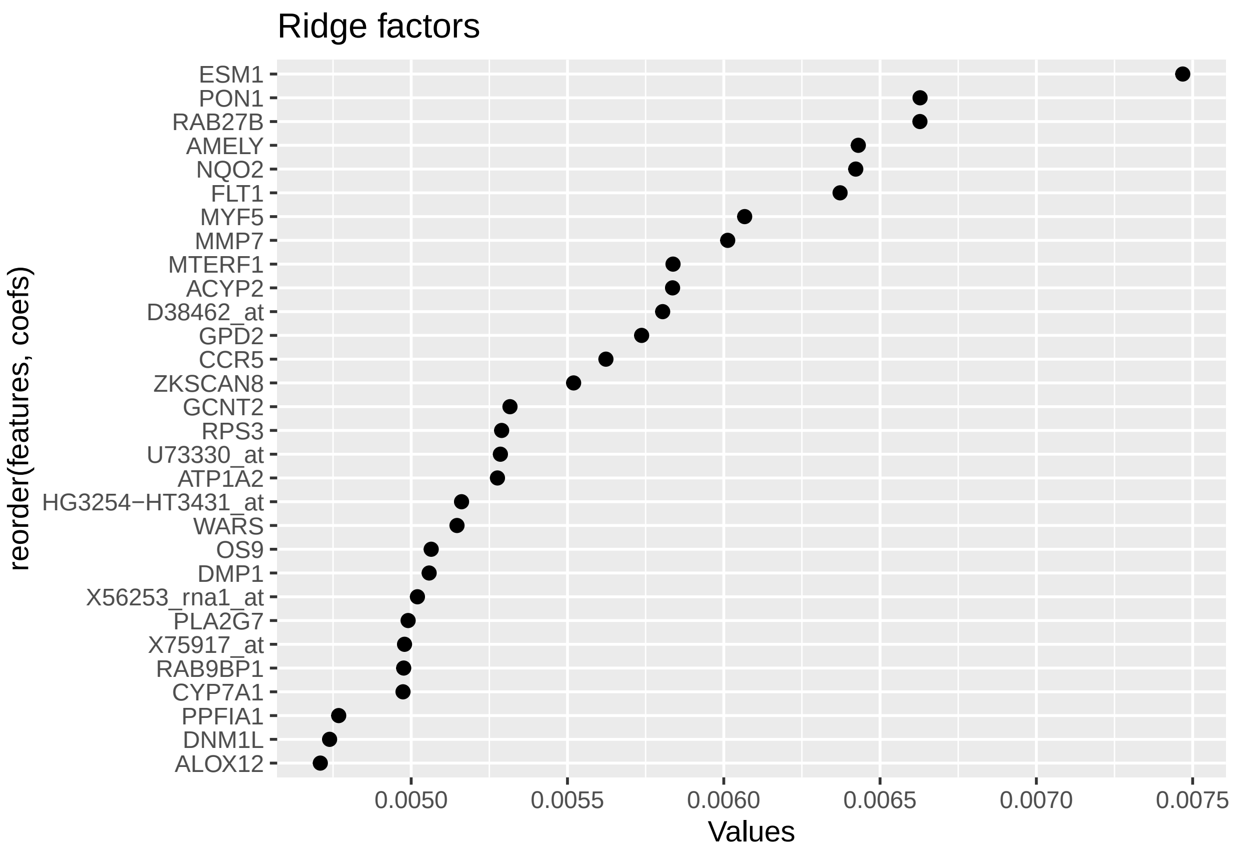
```
coef.ridge_sorted<-coef.ridge %>% arrange(-coefs)
coef.ridge_sorted<-coef.ridge_sorted[1:30,]


#making plots with values in descending order

ggplot(coef.enet,aes(x=coefs,y=reorder(features,coefs)))+geom_point(size=2)+ggtitle('Elastic Net factor
```



```
ggplot(coef.lasso,aes(x=coefs,y=reorder(features,coefs)))+geom_point(size=2)+ggtitle('LASSO factors')+la
```



```
ggplot(coef.ridge_sorted,aes(x=coefs,y=reorder(features,coefs)))+geom_point(size=2)+ggtitle('Ridge fact
```



```
#coefplot(fit.elastic_net,lambda='lambda.min',sort="magnitude")
#coefplot(fit.lasso,lambda='lambda.min',sort="magnitude")
#coefplot(fit.ridge,lambda='lambda.min',sort="magnitude")

a<-intersect(coef.ridge$features,coef.enet$features) #finding common coefficients between models
a<-intersect(a,coef.lasso$features)
```

It is interesting to note that non-zero factors between Elastic Net and LASSO follow roughly the same descending order, but that is not the case for Ridge. It can be seen that Elastic Net uses 32 significant coefficients, LASSO uses 17 and Ridge uses 7130.

```
#Fitting the models to the training data

mod.enet<-glmnet(X.train,y.train,alpha=0.5,family = "binomial",lambda=fit.elastic_net$lambda.min)
mod.lasso<-glmnet(X.train,y.train,alpha=1,family = "binomial",lambda=fit.lasso$lambda.min)
mod.ridge<-glmnet(X.train,y.train,alpha=0,family = "binomial",lambda=fit.ridge$lambda.min)


#Number of significant (non-zero) coefficients per model for the training set
```

The predictions will be analyzed using the package caret for determining the Confusion Matrix and other statistical information of the predictions.

```r
#Predictions on training data
prob.enet<-mod.enet %>% predict(newx=X.test,s=fit.elastic_net$lambda.min,type="response")
prob.lasso<-mod.lasso %>% predict(newx=X.test,s=fit.lasso$lambda.min,type="response")
prob.ridge<-mod.ridge %>% predict(newx=X.test,s=fit.ridge$lambda.min,type="response")

#Because from the contrast matrix level 0 is ALL and level 1 is AML, the probabilities will be re-coded

contrasts(y)
```

```
##     AML
## ALL   0
## AML   1
```

```r
pred.class.enet<-ifelse(prob.enet>0.5,"AML","ALL")
pred.class.lasso<-ifelse(prob.lasso>0.5,"AML","ALL")
pred.class.ridge<-ifelse(prob.ridge>0.5,"AML","ALL")


confusionMatrix(data=as.factor(pred.class.enet),reference=y.test)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction ALL AML
##        ALL  22   1
##        AML   1  12
##
##                Accuracy : 0.9444
##                  95% CI : (0.8134, 0.9932)
##     No Information Rate : 0.6389
##     P-Value [Acc > NIR] : 2.202e-05
##
##                   Kappa : 0.8796
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9565
##             Specificity : 0.9231
##          Pos Pred Value : 0.9565
##          Neg Pred Value : 0.9231
##              Prevalence : 0.6389
##          Detection Rate : 0.6111
##    Detection Prevalence : 0.6389
##       Balanced Accuracy : 0.9398
##
##        'Positive' Class : ALL
##
```

```r
confusionMatrix(data=as.factor(pred.class.lasso),reference=y.test)
```

```
## Confusion Matrix and Statistics
##
```

```
##           Reference
## Prediction ALL AML
##        ALL  22   1
##        AML   1  12
##
##                Accuracy : 0.9444
##                  95% CI : (0.8134, 0.9932)
##     No Information Rate : 0.6389
##     P-Value [Acc > NIR] : 2.202e-05
##
##                   Kappa : 0.8796
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9565
##             Specificity : 0.9231
##          Pos Pred Value : 0.9565
##          Neg Pred Value : 0.9231
##              Prevalence : 0.6389
##          Detection Rate : 0.6111
##    Detection Prevalence : 0.6389
##       Balanced Accuracy : 0.9398
##
##        'Positive' Class : ALL
##
```

```
confusionMatrix(data=as.factor(pred.class.ridge),reference=y.test)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction ALL AML
##        ALL  23   2
##        AML   0  11
##
##                Accuracy : 0.9444
##                  95% CI : (0.8134, 0.9932)
##     No Information Rate : 0.6389
##     P-Value [Acc > NIR] : 2.202e-05
##
##                   Kappa : 0.8754
##
##  Mcnemar's Test P-Value : 0.4795
##
##             Sensitivity : 1.0000
##             Specificity : 0.8462
##          Pos Pred Value : 0.9200
##          Neg Pred Value : 1.0000
##              Prevalence : 0.6389
##          Detection Rate : 0.6389
##    Detection Prevalence : 0.6944
##       Balanced Accuracy : 0.9231
##
##        'Positive' Class : ALL
```

```
##
```

```
#table(y.test,pred.class.enet)
#table(y.test,pred.class.lasso)
#table(y.test,pred.class.ridge)
#pred.class.enet<-ifelse(prob.enet>0.5,"ALL","AML")
#pred.class.lasso<-ifelse(prob.lasso>0.5,"AML","ALL")
#pred.class.ridge<-ifelse(prob.ridge>0.5,"AML","ALL")

#Misclassification error

1-mean(pred.class.enet==y.test)
```

```
## [1] 0.05555556
```

```
1-mean(pred.class.lasso==y.test)
```

```
## [1] 0.05555556
```

```
1-mean(pred.class.ridge==y.test)
```

```
## [1] 0.05555556
```

The results are similar with either model regarding accuracy (94.4%) and misclassification error (5.5%). It is interesting to note that virtually the same results can be obtained

```
real<-as.data.frame(y.test)
results<-cbind(pred.class.enet,pred.class.lasso,pred.class.ridge,real)
names(results)[1]<-"Elastic_Net"
names(results)[2]<-"LASSO"
names(results)[3]<-"Ridge"
names(results)[4]<-"Real_values"
results$subject<-rownames(results) #adding the correct subject number to each classification
view(results)
```

It can be seen that the Elastic Net and LASSO models misclassify observations 17 and 32. Patient/subject 17 is ALL but the models classify it as AML. Patient 32 is AML but is classified as ALL. The properly classified ALL and AML observations will be analyzed and compared with the misclassified results to determine the cause of the error.

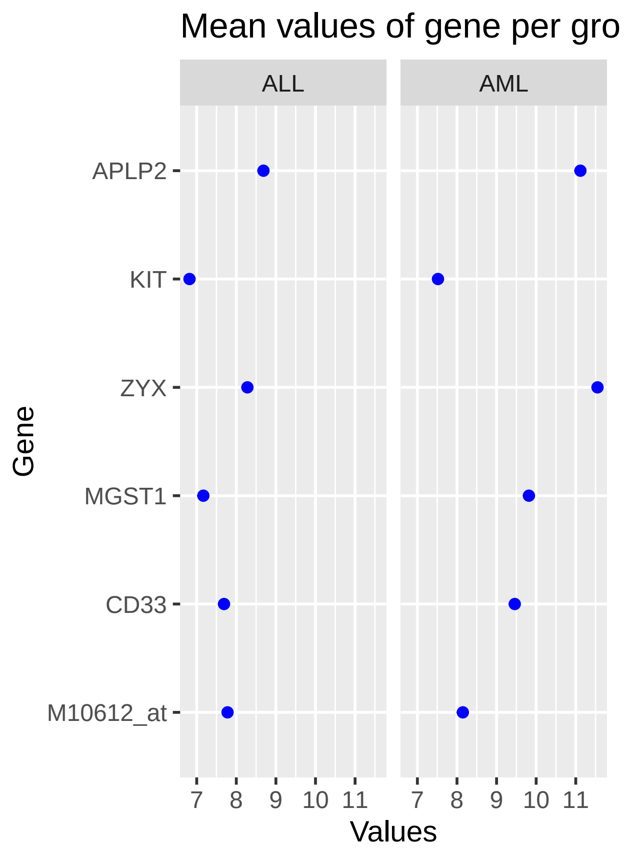
```
#Merging test data
test_dataset<-as.data.frame(X.test)
test_dataset<-cbind(results[,5],results[,4],test_dataset)
names(test_dataset)[1]<-"Subject" #renaming the columns
names(test_dataset)[2]<-"Class"

#Reshaping data
library(reshape)
```

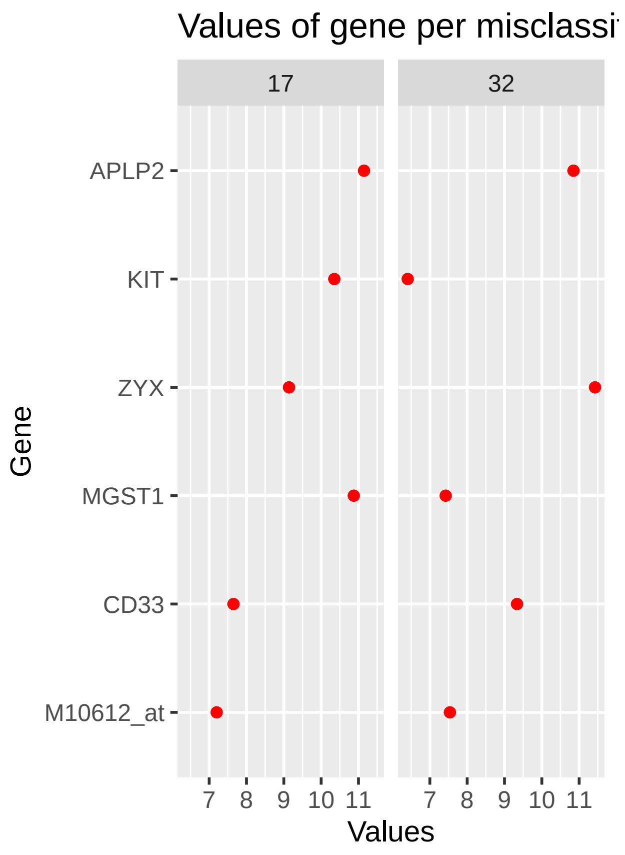
```
##
## Attaching package: 'reshape'
## The following object is masked from 'package:dplyr':
##
##     rename

## The following objects are masked from 'package:tidyr':
##
##     expand, smiths

## The following object is masked from 'package:Matrix':
##
##     expand
```

```
long<-melt(test_dataset,id=c("Subject","Class"))
names(long)[3]<-"Gene" #renaming the columns
names(long)[4]<-"Val"

means<-long %>% group_by(Gene,Class) %>% #calculating mean values for each gene per class
  summarise_at(vars(Val),funs(mean))
```

```
## Warning: `funs()` is deprecated as of dplyr 0.8.0.
## Please use a list of either functions or lambdas:
##
##   # Simple named list:
##   list(mean = mean, median = median)
##
##   # Auto named with `tibble::lst()`:
##   tibble::lst(mean, median)
##
##   # Using lambdas
##   list(~ mean(., trim = .2), ~ median(., na.rm = TRUE))
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was generated.
```

```
#Getting mean values for the most significant genes per group
sig_means<-means %>% filter(Gene %in% c("MGST1","KIT","M10612_at","APLP2","CD33","ZYX"))

#extracting values for the missclasified subjects
vals<-long %>% filter(Subject %in% c("17","32") & Gene %in%   c("MGST1","KIT","M10612_at","APLP2","CD33


g1<-ggplot(sig_means,aes(x=Val,y=Gene))+geom_point(color="Blue")+facet_wrap(~Class)+
  ggtitle("Mean values of gene per group")+labs(x='Values')

g2<-ggplot(vals,aes(x=Val,y=Gene))+geom_point(color="red")+facet_wrap(~Subject)+
  ggtitle("Values of gene per misclassified subject")+labs(x='Values')


library(ggpubr)

#Plotting results together

ggarrange(g1,g2,ncol=2,nrow=1)
```





Based on this analysis, it appears that the reason why subject 17 is misclassified as AML and subject 32 is misclassified as ALL is because the coefficients associated with the most important genes are closer to the mean values for the other class. It can be seen that the means for AML for the genes tend to be around 8 and up to about 12. The same spread pattern is seen in subject 17, although is classified as ALL. For subject 32 althought the data is more sparse it can be seen that the gene values are also below 9, similarly to the ALL group means, although subject 32 is classified as AML.

PART 2

LITERATURE REVIEW

Finding Online Extremists in Social Networks

Klausen et. al. https://arxiv.org/pdf/1610.06242.pdf

The paper by Klausen et al covers the use of machine learning algorithms to detect extremists on social media using behavioral and network features.The study collects large amounts of data from users from Twitter that have been identified that have some interaction with the extremist group ISIS (The Islamic State of Iraq and the Levant). The authors collected 1.3 million user profiles related to ISIS and their friends and followers, and 4.8 million tweets. Due to the large amount of collected data, it is clear that a machine learning approach is appropriate to analyze the data.

The first model the authors build is to use logistic regression to predict account suspensions using a dataset of 5,000 accounts. The predictors in this case were network and account features including followed accounts known to belong to ISIS, date and time, geo-location and others. It seems interesting to me the use of mixed variables (binary and numeric) to fit a logistic model.Their results suggest that using a ℓ_1 regularization the model can detect about 60% of the suspended users with a 10% false positivity rate. Misclassified accounts were identified as having few tweets or no posting content at all.

The next model of supervised machine learning approach was developed to detect if two user profiles belong to the same user.The similarity metrics used were:

-Screen name: Distance between two strings to identify similarly named accounts was used(The Levenshtein ratio). -Similarity between profile pictures using matching shade patterns. The model used 3,944 profiles and the classification was specified as 1 if profiles belonged to the same user and 0 if the they belonged to different users. A logistic regression with a ℓ_1 regularization with $\lambda = 10$ identified as the best regularization parameter using cross validation. Interestingly, feature with the highest regression coefficient was the Levenshtein ratio (7.05). In other words, the predictor with the highest regression coefficient is the one that relates to similarities in user name. It was expected that the classifier correctly identifies 80% of accounts pair belonging to the same user and that it would misclassify % of the different user pairs.

A refollowing model (to determine how users reconnect) was also developed. The model would predict the probability that a user will re-follow the same "friend" upon this person opens a new Twitter account. Here the data was clustered and the features were set as User0 (from a suspended user account) and Friend, the account that was to be followed.

The model used in this case was a quadratic kernel logistic regression, to accomodate interactions between the terms, allowing to linear fit in all terms. The data was divided between training, validation and test sets (50%, 25%, 25%). The regularization term λ was selected as 10^{-5} using the AUC criterion instead of cross validation. One major limitation of the quadratic kernel approach is that the expressions on the fit models are not easy to interpret, and the AUC approach for the model resulted in 0.66. The authors suggest that this indicates that there is a refollowing behavior that is beyond the users in the dataset.

The final model was developed to find the new account of a previously suspended user.This the most extensive section of the paper and probably the most important contribution of the authors to the field. They develop theorems to perform incorporate a stochastic search as the core of the model. This included derivations for conditional reconnection, and a *policy cost* or the cost of performing the search for the new account of a previously suspended user. This model was developed and tested on a much smaller number of accounts (169 pairs), where 15 were used for testing. Of key importance for this model was the probability for conditional existence $\rho(t)$, which uses a Bayesian approach. It was used with different policies as criterions on when the analysis would terminate.

In this case, the policies were: Optimal, Greedy, Min-N, Max-P. The most relevant policies where the Optimal and Greedy approaches. In the first case, the probability of finding a new account at each stage is maximized, and in the second the expected cost is minimized. These were the more relevant because the analysis showed that the costs for both approaches were very similar in most cases, which would indicate a minimization of cost and a maximizing the probability at each stage have the same effect.

Finally, the authors indicated that their models can be used beyond Twitter as the algorithms used behavioral and statistical approaches but are were not limited by a specific type of social network. It would be interesting to see how these models perform with models that have been developed specifically for each one of the major social networks (Instagram, Facebook and Twitter) and what predictors these specific models take into account to make the predictions. Overall I think the topic is quite interesting, as an user-based policing in social networks for extremists is certainly impossible in a world where billions of persons have accounts and each social networks has millions of features that can be exploited. This paper made me realize uses of statistical methods of machine learning to address this technological need.